C2: First detection of a *Mesonivirus* in *Culex pipens* in five countries around the Mediterranean basin

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Culex pipiens is a mosquito vector of West Nile virus (WNV), the causing agent of West Nile fever. Epizooties of WNV have taken place in Europe, mainly in France, Italy and Spain, and in some instances, human cases have been diagnosed. However, beyond WNV, little is known on the viruses associated to *Culex pipiens*, above all on viruses non-pathogenic for humans or livestock. Like *Wolbachia* bacteria, such viruses could have a role in WNV epidemiology either limiting mosquito populations or modulating the chances of WNV infection of *C. pipiens.*
Through metagenomics approach, we characterized the virome of *C. pipiens* in five countries around the Mediterranean basin

Our results show for the first time conserved patterns in diversity and structure within the virome of *C. pipiens* with a large abundance of the *Mesoniviridae*, a relatively new family of mosquito-specific viruses in the *Nidovirales* order. To date, the few data available on *Mesoniviridae* show that they probably have a worldwide distribution and they can infect different species of mosquitoes. The sequences obtained allowed to assemble several full genomes of *Mesoniviridae.* Interestingly, phylogenetic analysis showed a highly similarity with strains of *Nam-Dinh* virus, a virus recently identified in Côte d'Ivoire (West Africa) and Vietnam but which had not yet been observed in Europe. In view of the importance of the Mesoniviridae dispersion throughout the world, we determined the relative abundance of this family in natural population of *Culex pipiens* in Camargue.